RAW SEQUENCE LISTING ERROR REPORT
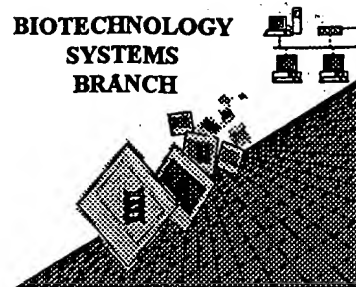
The Biotechnology Systems Branch of the Scientific and Technical Information Cente (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/218,913_

Art Unit / Team No. : _1652_

Date Processed by STIC: _5/19/2000_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEN WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

P. Jung

1652

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/218,913**

DATE: 05/19/2000
TIME: 17:32:29

Input Set: **I218913.RAW**

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1	<110>	Hall, Roderick L
2		Poll, Christopher T.
3		Newton, Benjamin B.
4		Taylor, William J.A.
5	<120>	A Method for Accelerating the Rate of Mucociliary Clearance
6	<130>	98,736
7	<140>	US/09/218,913
8	<141>	1998-12-22
9	<160>	71
10	<170>	Microsoft Word 97

ERRORED SEQUENCES FOLLOW

	11	<210> 11
E-->	12	<211> (170) /79 *shown*
	13	<212> PRT
	14	<213> Homo sapien
	15	<220>
	16	<221> peptide
	17	<222> 1..170
	18	<223> /note= "Xaa at positions 8, 17, 21-26, 40, 42, 45-47, 52, 64,
	19	103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any
	20	amino acid residue"
	21	<400> 11

what about Xaa at position 19?

```
W-->OK  22    Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val
        23    1               5                   10              15
W-->    24    Xaa Gly (Xaa) Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
        25                  20                  25              30
W--> OK 26    Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser
        27                  35                  40                  45
W--> OK 28    Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa
        29                  50                  55                  60
        30    Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
        31    65                  70                  75                  80
        32    Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
        33                        85                  90                  95
W--> OK 34    Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa
        35                        100                 105             110
W--> OK 36    Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
        37                  115                 120                 125
W--> OK 38    Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn
        39                  130                 135                 140
```

W--> 0(40   Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln
     41   145   150   155   160
     42   Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
     43   165   170   175
     44   Ala Val Ser

---

     45   <210> 16
E--> 46   <211> (428) 431 atms
     47   <212> DNA
     48   <213> Homo sapien
     49   <220>
     50   <221> misc_feature
     51   <222> 1..430
     52   <223> /note= "n at positions 3, 11, 12, 17, 51 and 429 represent any nucleic acid"
     53   <400> 16
W--OK 54   gcngcgcgtt nntcgcntgc tgggatcgct gctgcacctc tctggggtcg nggcggccga   60
     55   ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc   120
     56   ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg   180
     57   gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc   240
     58   cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc   300
     59   tgtcccaagt gctcccagaa ggcaggattc ttgaagacca cttcagcgat atgttcaact   360
     60   atgaagaata ctggcaccgc caacgcattc actgggcctg cgtgcatcct tcccacgctg   420
W--> 61   gtactttgnc g   431

---

     62   <210> 35
     63   <211> 36
     64   <212> DNA
     65   <213> Homo sapien
     66   <400> 35
E--> 67   ggtctagagg ccgggtcgtt tctcgcctgg ctggga   36 (37)

---

     68   <210> 54
E--> 69   <211> 23
     70   <212> (DNA) PRT
     71   <213> Homo sapien
     72   <220>
     73   <223> Human Bikunin protein fragment
     74   <400> 54
     75   Met Leu Arg Ala Glu Ala Asp Gly Asn Ser Arg Leu Leu Gly Ser Leu
     76   1   5   10   15
     77   Leu Leu Ser Gly Val Leu Ala
     78   20

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please r view the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Input Set: **I218913.RAW**

Line	?	Error/Warning	Original Text
12	E	Input 170, Calc Seq.Length 179 differ	<211> 170
22	W	"N" or "Xaa" used: Feature required	Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe C
24	W	"N" or "Xaa" used: Feature required	Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa T
26	W	"N" or "Xaa" used: Feature required	Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa G
28	W	"N" or "Xaa" used: Feature required	Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu L
34	W	"N" or "Xaa" used: Feature required	Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys T
36	W	"N" or "Xaa" used: Feature required	Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp T
38	W	"N" or "Xaa" used: Feature required	Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly C
40	W	"N" or "Xaa" used: Feature required	Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu A
46	E	Input 428, Calc# Bases 431 differ	<211> 428
54	W	"N" or "Xaa" used: Feature required	gcngcgcgtt nntcgcntgc tgggatcgct gctgcacc
61	W	"N" or "Xaa" used: Feature required	gtactttgnc g
67	E	Number of Bases conflict w/ Running Total	ggtctagagg ccgggtcgtt tctcgcctgg ctggga
69	E	Input 23, Calc# Bases 0 differ	<211> 23